

***Amendments to the Claims***

Claims 1-21 (canceled)

Claim 22 (new): A genetic vector for stable transfection and expression of a desired protein within eukaryotic cells comprising:

- (a) distal 5' flanking sequences of a eukaryotic locus;
- (b) proximal 5' regulatory sequences of a eukaryotic locus;
- (c) at least a first insertion site for a first heterologous coding sequence;

and

(d) proximal 3' regulatory sequences effective for transcription termination of a eukaryotic locus;

wherein said sequences are operably joined in order (a)-(d) in a 5' to 3' orientation, with optional linker sequences between adjacent sequences; and wherein

- (1) said distal 5' flanking sequences comprise a sequence of at least 100 bases having at least 70% identity to a nucleotide sequence found between 20 bp and 100,000 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus; or
- (2) said proximal 5' regulatory sequences comprise a sequence of at least 20 bases having at least 70% identity to a nucleotide sequence found between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus.

Claim 23 (new): A genetic vector for stable transfection and expression of a desired protein within eukaryotic cells comprising:

- (a) distal 5' flanking sequences of a eukaryotic locus;
- (b) proximal 5' regulatory sequences of a eukaryotic locus;
- (c) at least a first heterologous coding sequence encoding said desired protein; and
- (d) proximal 3' regulatory sequences effective for transcription termination of a eukaryotic locus;

wherein said sequences are operably joined in order (a)-(d) in a 5' to 3' orientation, with optional linker sequences between adjacent sequences; and wherein

- (1) said distal 5' flanking sequences comprise a sequence of at least 100 bases having at least 70% identity to a nucleotide sequence found between 20 bp and 100,000 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus; or
- (2) said proximal 5' regulatory sequences comprise a sequence of at least 20 bases having at least 70% identity to a nucleotide sequence found between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus.

Claim 24 (new): A genetic vector of claim 22 wherein said distal 5' flanking sequences are derived from a ferritin heavy chain locus.

Claim 25 (new): A genetic vector of claim 22 wherein said proximal 5' regulatory sequences are derived from a ferritin heavy chain locus.

Claim 26 (new): A genetic vector of claim 22 wherein said proximal 5' regulatory sequences and said 5' distal flanking sequences are derived from a ferritin heavy chain locus.

Claim 27 (new): A genetic vector of claim 22 wherein said proximal 3' regulatory sequences are derived from a ferritin heavy chain locus.

Claim 28 (new): A genetic vector of claim 22 further comprising distal 3' flanking sequences of a ferritin heavy chain locus.

Claim 29 (new): A genetic vector of claim 22 wherein said insertion site for a heterologous sequence includes at least one restriction endonuclease site.

Claim 30 (new): A genetic vector as in claim 29 wherein said insertion site for a heterologous sequence is a polylinker site including at least two restriction endonuclease sites.

Claim 31 (new): A genetic vector of claim 22 wherein said proximal 5' regulatory sequences include a eukaryotic intron sequence.

Claim 32 (new): A genetic vector as in claim 31 wherein said eukaryotic intron sequence is derived from intron 1 of a ferritin heavy chain gene.

Claim 33 (new): A genetic vector of claim 22 wherein said proximal 5' regulatory sequences include untranslated exon sequences.

Claim 34 (new): A genetic vector of claim 22 wherein said distal 5' flanking sequences and said proximal 5' regulatory sequences have a total length of between 1,000 and 10,000 bases.

Claim 35 (new): A genetic vector of claim 22 wherein said proximal 3' regulatory sequences and any distal 3' flanking sequences have a total length of between 1,000 and 10,000 bases.

Claim 36 (new): A genetic vector of claim 22 wherein said distal 5' flanking sequences comprise a sequence having at least 80% identity to said nucleotide sequence found between 20 bp and 100,000 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus.

Claim 37 (new): A genetic vector of claim 22 wherein said distal 5' flanking sequences comprise a sequence having at least 90% identity to said nucleotide sequence found between 20 bp and 100,000 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus.

Claim 38 (new): A genetic vector of claim 22 wherein said distal 5' flanking sequences comprise a sequence having 100% identity to said nucleotide sequence found

between 20 bp and 100,000 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus.

Claim 39 (new): A genetic vector of claim 22 wherein said distal 5' flanking sequences comprise a sequence of at least 500 bases having at least 70% identity to said nucleotide sequence found between 20 bp and 100,000 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus.

Claim 40 (new): A genetic vector of claim 22 wherein said distal 5' flanking sequences comprise a sequence of at least 1,000 bases having at least 70% identity to said nucleotide sequence found between 20 bp and 100,000 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus.

Claim 41 (new): A genetic vector of claim 22 wherein said proximal 5' regulatory sequences comprise a sequence having at least 80% identity to said nucleotide sequence found between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus.

Claim 42 (new): A genetic vector of claim 22 wherein said proximal 5' regulatory sequences comprise a sequence having at least 90% identity to said nucleotide sequence found between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus.

Claim 43 (new): A genetic vector of claim 22 wherein said proximal 5' regulatory sequences comprise a sequence having 100% identity to said nucleotide sequence found between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus.

Claim 44 (new): A genetic vector of claim 22 wherein said proximal 5' regulatory sequences comprise a sequence of at least 500 bases having at least 70% identity to said nucleotide sequence found between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus.

Claim 45 (new): A genetic vector of claim 22 wherein said proximal 5' regulatory sequences comprise a sequence of at least 1,000 bases having at least 70% identity to said nucleotide sequence found between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus.

Claim 46 (new): A genetic vector of claim 22 wherein the length of said first insertion site is 0, 1, 2 or 3 bp.

Claim 47 (new): A genetic vector of claim 22 wherein the length of said first insertion site is 4 bp.

Claim 48 (new): A genetic vector of claim 22 wherein the length of said first insertion site is 1,000 bp.

Claim 49 (new): A genetic vector of claim 22 wherein the length of said first insertion site is 5,000 bp.

Claim 50 (new): A genetic vector of claim 22 wherein said proximal 3' regulatory sequences comprise a sequence having at least 70% identity to a nucleotide sequence found within the proximal 3' regulatory sequences of a ferritin heavy chain locus.

Claim 51 (new): A genetic vector of claim 22 wherein said proximal 3' regulatory sequences comprise a sequence having at least 80% identity to a nucleotide sequence found within the proximal 3' regulatory sequences of a ferritin heavy chain locus.

Claim 52 (new): A genetic vector of claim 22 wherein said proximal 3' regulatory sequences comprise a sequence having at least 90% identity to a nucleotide sequence found within the proximal 3' regulatory sequences of a ferritin heavy chain locus.

Claim 53 (new): A genetic vector of claim 22 wherein said proximal 3' regulatory sequences comprise a sequence having 100% identity to a nucleotide sequence found within the proximal 3' regulatory sequences of a ferritin heavy chain locus.

Claim 54 (new): A genetic vector of claim 22 wherein said proximal 3' regulatory sequences comprise at least 10 nucleotides.

Claim 55 (new): A genetic vector of claim 22 wherein said proximal 3' regulatory sequences comprise at least 1,000 nucleotides.

Claim 56 (new): A genetic vector of claim 22 wherein said proximal 3' regulatory sequences consist essentially of a polyadenylation signal.

Claim 57 (new): A genetic vector of claim 22 further comprising a distal 3' flanking sequence of a eukaryotic locus comprising a sequence of at least 100 bases having at least 70% identity to a nucleotide sequence found within the distal 3' flanking sequences of a ferritin heavy chain locus.

Claim 58 (new): A genetic vector of claim 57 wherein said distal 3' flanking sequence comprises a sequence having at least 80% identity to said nucleotide sequence found within the distal 3' flanking sequences of a ferritin heavy chain locus.

Claim 59 (new): A genetic vector as in claim 57 wherein said distal 3' flanking sequence comprises a sequence having at least 90% identity to said nucleotide sequence found within the distal 3' flanking sequences of a ferritin heavy chain locus.

Claim 60 (new): A genetic vector as in claim 57 wherein said distal 3' flanking sequence comprises a sequence having 100% identity to said nucleotide sequence found within the distal 3' flanking sequences of a ferritin heavy chain locus.

Claim 61 (new): A genetic vector as in claim 57 wherein said distal 3' flanking sequence comprises a sequence of at least 500 bases having at least 70% identity to said nucleotide sequence found within the distal 3' flanking sequences of a ferritin heavy chain locus.

Claim 62 (new): A genetic vector as in claim 57 wherein said distal 3' flanking sequence comprises a sequence of at least 1,000 bases having at least 70% identity to said nucleotide sequence found within the distal 3' flanking sequences of a ferritin heavy chain locus.

Claim 63 (new): The genetic vector pFerX8.

Claim 64 (new): The genetic vector pFerX11.

Claim 65 (new): A eukaryotic cell transfected with a vector of claim 22.

Claim 66 (new): A eukaryotic cell of claim 65 wherein said vector has stably integrated into a chromosome of a said cell.

Claim 67 (new): A eukaryotic cell of claim 65 wherein said first coding sequence is expressed in said cell.

Claim 68 (new): A eukaryotic cell comprising:

- (a) distal 5' flanking sequences of a eukaryotic locus;
- (b) proximal 5' regulatory sequences of a eukaryotic locus;
- (c) at least a first coding sequence; and
- (d) proximal 3' regulatory sequences effective for transcription

termination of a eukaryotic locus;

wherein said sequences are operably joined in order (a)-(d) in a 5' to 3' orientation, with optional linker sequences between adjacent sequences; and wherein

- (1) said distal 5' flanking sequences comprise an exogenous sequence of at least 100 bases having at least 70% identity to a nucleotide sequence found between 20 bp and 100,000 bp 5' of a transcriptional initiation site of a ferritin heavy chain locus; or
- (2) said proximal 5' regulatory sequences comprise an exogenous sequence of at least 20 bases having at least 70% identity to a nucleotide sequence found between 1 bp and 10,000 bp 5' of a translational initiation codon of a ferritin heavy chain locus.

Claim 69 (new): A eukaryotic cell comprising:

an exogenous 5' distal flanking sequence derived from a ferritin heavy chain locus operably joined to a coding sequence.

Claim 70 (new): A method of producing a desired protein in a eukaryotic cell comprising:

- (a) providing at least one cell of claim 65 or a descendent thereof;
- (b) maintaining said cell in a culture under conditions which permit high expression of said desired protein; and
- (c) isolating said desired protein from said culture.